## 5 **CLAIMS**

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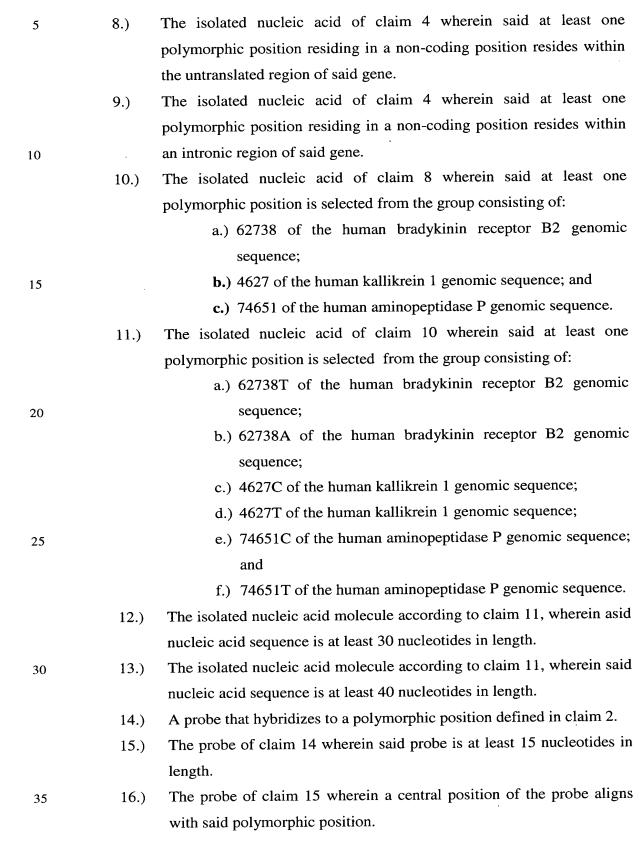
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## What is Claimed Is:

- 1.) An isolated nucleic acid derived from a human gene encoding a protein selected from a member of the group consisting of aminopeptidase P protein (XPNPEP2), bradykinin receptor B1 protein (BDKRB1), tachykinin receptor 1 protein (TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein (KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein (PI4), wherein said nucleic acid comprises at least one polymorphic position.
- The isolated nucleic acid of claim 1 wherein said at least one 2.) polymorphic position for each said gene is a polymorphic position specified in Table V, or complement thereof.
- 3.) The isolated nucleic acid of claim 2 wherein the sequence at said at least one polymorphic position is depicted in a nucleic acid sequence selected from the group consisting of SEQ ID NO: 163 to 288; 643 to 706; and 910 to 961, and 1574 to 1575, or complement thereof.
- 4.) The isolated nucleic acid of claim 3 wherein said at least one polymorphic position resides in a non-coding position within the genomic sequence of said gene.
- The isolated nucleic acid of claim 3 wherein said at least one 5.) polymorphic position resides in a coding position within the genomic sequence of said gene.
- 6.) The isolated nucleic acid of claim 5 wherein said at least one polymorphic position residing in a coding position results in a missense mutation of the translated product of said gene.
- 7.) The isolated nucleic acid of claim 5 wherein said at least one polymorphic position residing in a coding position results in a silent mutation of the translated product of said gene.



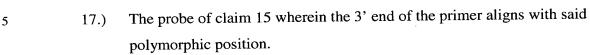
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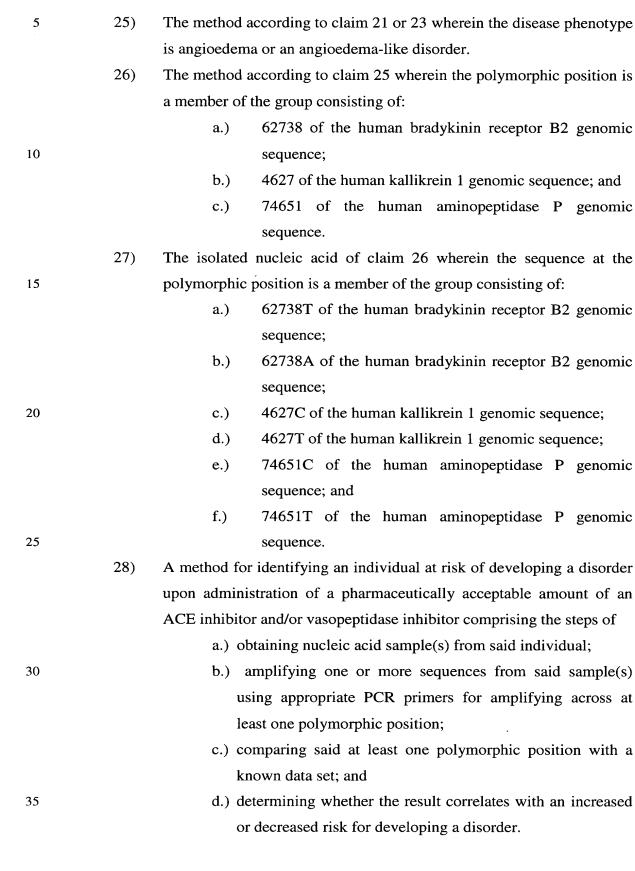
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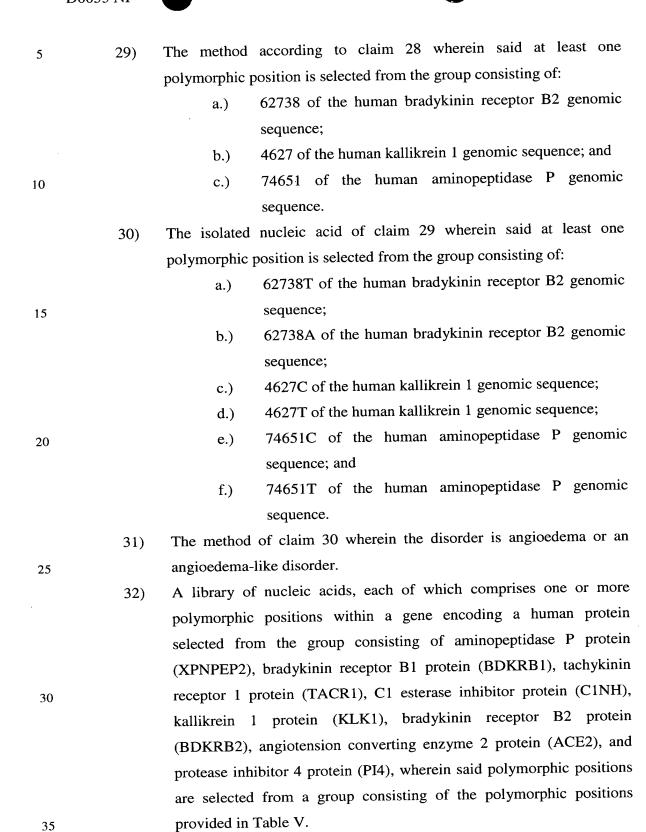
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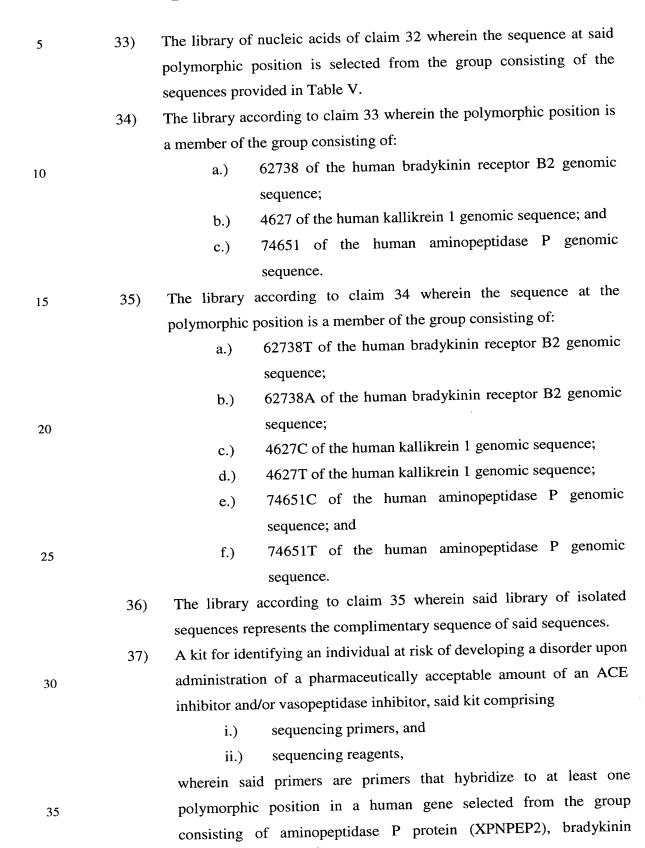
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- 18.) A method of analyzing at least one nucleic acid sample, comprising the steps of (1) obtaining said nucleic acid sample from one or more individuals; and (2) determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group consisting of aminopeptidase P protein (XPNPEP2), bradykinin receptor B1 protein (BDKRB1), tachykinin receptor 1 protein (TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein (KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein (PI4).
- 19.) The method according to claim 18, further comprising the steps of (3) testing each individual for the presence of a disease phenotype; and (4) correlating the presence of the disease phenotype with the sequence at said one or more polymorphic positions.
- 20.) The method according to claim 19, wherein said one or more polymorphic position of said nucleic acid sequence is a polymorphic position specified in Table V for said gene.
- 21.) The method according to claim 20, wherein the nucleic acid sequence at said one or more polymorphic position is depicted in a nucleic acid sequence selected from the group consisting of SEQ ID NO:163 to 288; 643 to 706; and 910 to 961, and 1574 to 1575, or complement thereof.
- 22.) A method of constructing haplotypes using the isolated nucleic acids of claim 1, comprising the step of grouping at least two said nucleic acids.
- 23.) The method according to claim 22 further comprising the step of using said haplotypes to identify an individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with said haplotype.
- The method according to claim 19 further comprising the step of quantifying the nucleic acid sample comprising the polymorphic base.







5		receptor B1 protein (BDKRB1), tachykinin receptor 1 protein
		(TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein
		(KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension
		converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein
		(PI4).
10	38)	The kit according to claim 37 wherein said polymorphic positions are
10	20)	selected from a group consisting of the polymorphic positions provided
		in Table V.
	39)	The kit according to claim 38 wherein the polymorphic position is a
	37)	member of the group consisting of:
15		a.) 62738 of the human bradykinin receptor B2 genomic
15		sequence;
		b.) 4627 of the human kallikrein 1 genomic sequence; and
		c.) 74651 of the human aminopeptidase P genomic
		sequence.
20	40)	The kit according to claim 39 wherein the sequence at the polymorphic
20	40)	position is a member of the group consisting of:
		a.) 62738T of the human bradykinin receptor B2 genomic
		sequence;
		b.) 62738A of the human bradykinin receptor B2 genomic
25		sequence;
23		c.) 4627C of the human kallikrein 1 genomic sequence;
		d.) 4627T of the human kallikrein 1 genomic sequence;
		e.) 74651C of the human aminopeptidase P genomic
		sequence; and
30		f.) 74651T of the human aminopeptidase P genomic
50		sequence.
	41)	The kit according to claim 40 wherein said primer(s) hybridizes
	71)	The way approved to comment to the Francisco and the comments of the comments

immediately adjacent to said polymorphic positions.

E	42) The kit according to claim 41 wherein said primer(s) hybridizes to said
5	polymorphic positions such that the central position of the primer
	aligns with the polymorphic position of said gene.
	1: 4. slaim 28 further comprising the step of
	subjecting the product(s) of said amplification to a genetic bit analysis
	(GBA) reaction.
10	a control of the second strick of developing a disorder
	44) A method for identifying an individual at risk of developing a partial upon administration of a pharmaceutically acceptable amount of an
	ACE inhibitor and/or vasopeptidase inhibitor comprising the steps of
	the same of the sa
	at least one
15	b.) determining the nucleotide present at least one polymorphic position,
	the state of the s
	c.) comparing said at least one polymorphic position with a known data set; and
	the state of the correlates with an
	d.) determining whether the result correlates with an increased or decreased risk for developing a disorder.
20	the slaim 44 wherein said at least one
	polymorphic position is selected from the group consisting of:
	and a second sec
	a.) 62738 of the human bradykinin receptor B2 generally sequence;
	b.) 4627 of the human kallikrein 1 genomic sequence; and
25	c.) 74651 of the human aminopeptidase P genomic
	sequence.
	1 : 1 - f alaim 45 wherein said at least one
	polymorphic position is selected from the group consisting of:
- 0	a.) 62738T of the human bradykinin receptor B2 genomic
30	sequence;
	b.) 62738A of the human bradykinin receptor B2 genomic
	sequence;
	c.) 4627C of the human kallikrein 1 genomic sequence;
25	d.) 4627T of the human kallikrein 1 genomic sequence;
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5	e.) 74651C of the human aminopeptidase P genomic
	sequence; and
	f.) 74651T of the human aminopeptidase P genomic
	sequence.
	47) The method of claim 46 wherein the disorder is angioedema or an
10	angioedema-like disorder.
	A method for genotyping an individual comprising the steps of
	a.) obtaining a nucleic acid sample(s) from said individual;
	b.) determining the nucleotide present at least one
	polymorphic position, and
15	c.) comparing said at least one polymorphic position with a
	known data set.
	49) The method according to claim 48 wherein said at least one
	polymorphic position is selected from the group consisting of:
	a.) 62738 of the human bradykinin receptor B2 genomic
20	sequence;
	b.) 4627 of the human kallikrein 1 genomic sequence; and
	c.) 74651 of the human aminopeptidase P genomic
	sequence.
	50) The isolated nucleic acid of claim 49 wherein said at least one
25	polymorphic position is selected from the group consisting of:
	a.) 62738T of the human bradykinin receptor B2 genomic
	sequence;
	b.) 62738A of the human bradykinin receptor B2 genomic
	sequence;
30	c.) 4627C of the human kallikrein 1 genomic sequence;
	d.) 4627T of the human kallikrein 1 genomic sequence;
	e.) 74651C of the human aminopeptidase P genomic
	sequence; and
	f.) 74651T of the human aminopeptidase P genomic
35	sequence.